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Search for Limits Show: ☐ 1: Q96JB6. Lysyl oxidase hom...[gi:20177960]

BLink, Domains, Links

LOCUS Q96JB6 756 aa linear PRI 15-JUN-2004

DEFINITION Lysyl oxidase homolog 4 precursor (Lysyl oxidase-like protein 4)
(Lysyl oxidase related protein C).

ACCESSION Q96JB6

VERSION Q96JB6 GI:20177960

DBSOURCE swissprot: locus LOL4_HUMAN, accession Q96JB6;

class: standard.

extra accessions:Q96DY1,Q96PC0,Q9H6T5,created: Feb 28, 2003.

sequence updated: Feb 28, 2003.

annotation updated: Jun 15, 2004.

xrefs: gi: 14669470, gi: 14669471, gi: 17861371, gi: 17861372, gi:
16660130, gi: 16660131, gi: 14043078, gi: 14043079, gi: 15341930,
gi: 15341931, gi: 10438090, gi: 10438091xrefs (non-sequence databases): GenewHGNC:17171, MIM 607318,
InterProIPR001695, InterProIPR001190, PfamPF01186, PfamPF00530,
PRINTSPR00074, PRINTSPR00258, ProDomPD013887, SMARTSM00202,
PROSITEPS00926, PROSITEPS00420, PROSITEPS50287

KEYWORDS Oxidoreductase; Copper; Glycoprotein; Repeat; Signal; LTQ.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiensEukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (residues 1 to 756)

AUTHORS Ito,H., Akiyama,H., Iguchi,H., Iyama,K., Miyamoto,M., Ohsawa,K. and
Nakamura,T.TITLE Molecular cloning and biological activity of a novel lysyl
oxidase-related gene expressed in cartilage

JOURNAL J. Biol. Chem. 276 (26), 24023-24029 (2001)

MEDLINE 21316447

PUBMED 11292829

REMARK SEQUENCE FROM N.A.

TISSUE=Testis

REFERENCE 2 (residues 1 to 756)

AUTHORS Maki,J.M., Tikkanen,H. and Kivirikko,K.I.

TITLE Cloning and characterization of a fifth human lysyl oxidase
isoenzyme: the third member of the lysyl oxidase-related subfamily
with four scavenger receptor cysteine-rich domains

JOURNAL Matrix Biol. 20 (7), 493-496 (2001)

MEDLINE 21550107

PUBMED 11691589

REMARK SEQUENCE FROM N.A.

REFERENCE 3 (residues 1 to 756)

AUTHORS Asuncion,L., Fogelgren,B., Fong,K.S., Fong,S.F., Kim,Y. and
Csiszar,K.TITLE A novel human lysyl oxidase-like gene (LOXL4) on chromosome 10q24
has an altered scavenger receptor cysteine rich domain

JOURNAL Matrix Biol. 20 (7), 487-491 (2001)

MEDLINE 21550106

PUBMED 11691588

REMARK SEQUENCE FROM N.A.
TISSUE=Placenta

REFERENCE 4 (residues 1 to 756)

AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

MEDLINE 22388257

PUBMED 12477932

REMARK SEQUENCE FROM N.A.
TISSUE=Eye

REFERENCE 5 (residues 1 to 756)

AUTHORS Ota,T., Suzuki,Y., Nishikawa,T., Otsuki,T., Sugiyama,T., Irie,R., Wakamatsu,A., Hayashi,K., Sato,H., Nagai,K., Kimura,K., Makita,H., Sekine,M., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T., Ishii,S., Yamamoto,J., Saito,K., Kawai,Y., Isono,Y., Nakamura,Y., Nagahari,K., Murakami,K., Yasuda,T., Iwayanagi,T., Wagatsuma,M., Shiratori,A., Sudo,H., Hosoiri,T., Kaku,Y., Kodaira,H., Kondo,H., Sugawara,M., Takahashi,M., Kanda,K., Yokoi,T., Furuya,T., Kikkawa,E., Omura,Y., Abe,K., Kamihara,K., Katsuta,N., Sato,K., Tanikawa,M., Yamazaki,M., Ninomiya,K., Ishibashi,T., Yamashita,H., Murakawa,K., Fujimori,K., Tanai,H., Kimata,M., Watanabe,M., Hiraoka,S., Chiba,Y., Ishida,S., Ono,Y., Takiguchi,S., Watanabe,S., Yosida,M., Hotuta,T., Kusano,J., Kanehori,K., Takahashi-Fujii,A., Hara,H., Tanase,T.O., Nomura,Y., Togiya,S., Komai,F., Hara,R., Takeuchi,K., Arita,M., Imose,N., Musashino,K., Yuuki,H., Oshima,A., Sasaki,N., Aotsuka,S., Yoshikawa,Y., Matsunawa,H., Ichihara,T., Shiohata,N., Sano,S., Moriya,S., Momiyama,H., Satoh,N., Takami,S., Terashima,Y., Suzuki,O., Nakagawa,S., Senoh,A., Mizoguchi,H., Goto,Y., Shimizu,F., Wakebe,H., Hishigaki,H., Watanabe,T., Sugiyama,A., Takemoto,M., Kawakami,B., Yamazaki,M., Watanabe,K., Kumagai,A., Itakura,S., Fukuzumi,Y., Fujimori,Y., Komiyama,M., Tashiro,H., Tanigami,A., Fujiwara,T., Ono,T., Yamada,K., Fujii,Y., Ozaki,K., Hirao,M., Ohmori,Y., Kawabata,A., Hikiji,T., Kobatake,N., Inagaki,H., Ikema,Y., Okamoto,S., Okitani,R., Kawakami,T., Noguchi,S., Itoh,T., Shigeta,K., Senba,T., Matsumura,K., Nakajima,Y., Mizuno,T., Morinaga,M., Sasaki,M., Togashi,T., Oyama,M., Hata,H., Watanabe,M., Komatsu,T., Mizushima-Sugano,J., Satoh,T., Shirai,Y., Takahashi,Y., Nakagawa,K., Okumura,K., Nagase,T., Nomura,N., Kikuchi,H., Masuho,Y., Yamashita,R., Nakai,K., Yada,T., Nakamura,Y., Ohara,O., Isogai,T. and Sugano,S.

TITLE Complete sequencing and characterization of 21,243 full-length human cDNAs

JOURNAL Nat. Genet. 36 (1), 40-45 (2004)
PUBMED [14702039](#)
REMARK SEQUENCE OF 492-756 FROM N.A.
COMMENT -----

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[FUNCTION] May modulate the formation of a collagenous extracellular matrix.
[COFACTOR] Copper and LTQ (By similarity).
[SUBCELLULAR LOCATION] Extracellular (Potential).
[TISSUE SPECIFICITY] Expressed in many tissues, the highest levels among the tissues studied being in the skeletal muscle, testis and pancreas. Expressed in cartilage.
[PTM] The lysine tyrosylquinone cross-link (LTQ) is generated by condensation of the epsilon-amino group of a lysine with a topaquinone produced by oxidation of tyrosine.
[SIMILARITY] Belongs to the lysyl oxidase family.
[SIMILARITY] Contains 4 SRCR domains.

FEATURES Location/Qualifiers
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 gene 1..756
 /gene="LOXL4"
 /note="synonym: LOXC"
 Protein 1..756
 /gene="LOXL4"
 /product="Lysyl oxidase homolog 4 precursor"
 /EC_number="1.4.3.-"
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 /gene="LOXL4"
 /region_name="Signal"
 /note="Potential."
 Region 3
 /gene="LOXL4"
 /region_name="Conflict"
 /note="W -> R (in Ref. 4)."
 Region 25..756
 /gene="LOXL4"
 /region_name="Mature chain"
 /note="Lysyl oxidase homolog 4."
 Region 32..133
 /gene="LOXL4"
 /region_name="Domain"
 /note="SRCR 1."
 Region 32..132
 /gene="LOXL4"
 /region_name="Scavenger receptor Cys-rich"
 /note="SR"
 /db_xref="CDD:178"
 Region 101
 /gene="LOXL4"
 /region_name="Conflict"
 /note="R -> Q (in Ref. 4)."
 Region 159..287
 /gene="LOXL4"

Region /region_name="Domain"
/note="SRCR 2."
174..286
/gene="LOXL4"
/region_name="Scavenger receptor Cys-rich"
/note="SR"
/db_xref="CDD:178"

Site 198
/gene="LOXL4"
/site_type="glycosylation"
/note="N-linked (GlcNAc...) (Potential)."

Region 311..411
/gene="LOXL4"
/region_name="Domain"
/note="SRCR 3."

Region 311..411
/gene="LOXL4"
/region_name="Scavenger receptor Cys-rich"
/note="SR"
/db_xref="CDD:178"

Region 405
/gene="LOXL4"
/region_name="Conflict"
/note="D -> A (in Ref. 4)."

Region 421..529
/gene="LOXL4"
/region_name="Domain"
/note="SRCR 4."

Region 421..528
/gene="LOXL4"
/region_name="Scavenger receptor Cys-rich"
/note="SR"
/db_xref="CDD:178"

Region 493
/gene="LOXL4"
/region_name="Conflict"
/note="S -> G (in Ref. 3)."

Region 533..736
/gene="LOXL4"
/region_name="Lysyl oxidase"
/note="Lysyl oxidase"
/db_xref="CDD:7932"

Region 533..736
/gene="LOXL4"
/region_name="Domain"
/note="Lysyl-oxidase like."

Region 539
/gene="LOXL4"
/region_name="Conflict"
/note="A -> T (in Ref. 3)."

Region 542
/gene="LOXL4"
/region_name="Conflict"
/note="V -> A (in Ref. 3)."

Site 611
/gene="LOXL4"
/site_type="metal-binding"
/note="Copper (Potential)."

Site 613
/gene="LOXL4"

Site /site_type="metal-binding"
/note="Copper (Potential)."
615
/gene="LOXL4"
/site_type="metal-binding"
/note="Copper (Potential)."
Site 629
/gene="LOXL4"
/site_type="glycosylation"
/note="N-linked (GlcNAc...) (Potential)."
Bond bond(638,674)
/gene="LOXL4"
/bond_type="xlink"
/note="Lysine tyrosylquinone (Lys-Tyr) (By similarity)."
Site 674
/gene="LOXL4"
/site_type="modified"
/note="2',4',5'-topaquinone (By similarity)."
Region 703
/gene="LOXL4"
/region_name="Conflict"
/note="Y -> H (in Ref. 3)."

ORIGIN

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121 dcshsedvgv ichprhrhrgy lsetvsnalq pqgrrleevr lkpilasakq hspvtegave
181 vkyeghwrqv cdqgwtmnns rvvcgmlgfp sevpvdshyy rkvwdlkmrd pksrlksltn
241 knsfwihqvt clgtephman cqvqvaparg klrpacpggm havvscvagp hfrppktpq
301 rkgsuaeepv vrlrsgaqvg egrvevlmnr qwgtvcdhrw nlisasvvr qlgfgsarea
361 lfgarlgqgl gpahlsevr rgyertlsdc palegsqngc qhendaavrc nvpmngfqng
421 vrlaggripe egllevqvev ngvprwgsvc senwglteam vacrqlglgf aihayketwf
481 wsgtpragev vmvgvrsgt elalqqcqrh gpvhcshggg rflagvscmd sapdlvmnaq
541 lvqetayled rplsqglycah eenclsksad hmdwpygyrr llrfstqiyn lgrtdfrpkt
601 grdswvwhqc hrhyhsievf thydlltng skvaeghkas fcledtncpt glqrryacan
661 fgeggvtvgc wdtyrhdidc qwvdtidvgp gnyifqvivn phyevaesdf snnmlqcrck
721 ydghrvwlhn chtgnsypan aelsleqeqr lrnnli
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Oct 4 2004 14:35:49